## SEQUENCE LISTING

- (1) GENERAL INFORMATION:
  - (i) APPLICANT: (other than US) WESTERN HEALTH CARE NETWORK (US only): LOCARNINI, S A, BARTHOLMEUSZ, A I, De MAN, R.
  - (ii) TITLE OF INVENTION: VIRAL VARIANTS AND METHODS FOR DETECTING SAME
  - (iii) NUMBER OF SEQUENCES: 20
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE\DAVIES COLLISON CAVE
    - (B) STREET: 1 LITTLE COLLINS STREET
    - (C) CITY: MELBOURNE
    - (D) STATE: VICTORÍA
    - (E) COUNTRY: AUSTRALIA
    - (F) ZIP: 3000
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: INTERNATIONAL (PCT)
    - (B) FILING DATE:15-AUG-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: AU PROVISIONAL
  - (B) FILING DATE: 08-NOV-1996
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: HUGHES DR, E JOHN L
  - (C) REFERENCE/DOCKET NUMBER: EJH/AF
- (ix) TELECOMMUNICATION INFORMATION: .
  - (A) TELEPHONE: +61 3 9254 2777
  - (B) TELEFAX: +61 3 9254 2770

- 28 -

17

GCT CCA AAT TCT TTA TA

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(2)	INFORMATION FOR SEQ ID NO:1:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
GGA	GTG TGG ATT CGC ACT CC	20
(2)	INFORMATION FOR SEQ ID NO:2:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 17 base pairs  (B) TYRE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	••
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
GCT	CCA AAT TCT TTA TA	17
(2)	INFORMATION FOR SEQ/ID NO:3:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 20 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS; single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
CCT	TTA CCC CGT TGC CCG GC	20
(2)	INFORMATION FOR SEQ ID NO:4:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 17 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO.4:	

23

20

- 29 -

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: 23 GCC GCG TCG CAG\AAG ATC TCA AT (2) INFORMATION FOR SEQ ID NO:6: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: hucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY\ linear (ii) MOLECULE TYPE: DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6: 20 GGT TCT ATC CTA ACC TTA CC (2) INFORMATION FOR SEQ ID NO. 7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (xi) SEQUENCE DESCRIPTION: SEQ ID\NO:7: GCC TCA TTT TGT GGG TCA CCA TA (2) INFORMATION FOR SEQ ID NO:8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: 21 TGG GGG TGG AGC CCT CAG GCT (2) INFORMATION FOR SEQ ID NO:9: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid STRANDEDNESS: single (C) (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA

Printed from Mimosa

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAC AAC ATT CCA CCA AGC TC

21

	- 30 -	
	\	
(2)	INFORMATION FOR SEQ ID NO:10:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLEQULE TYPE: DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
AAA	TTC GCA GTC CC AAC	18
(2)	INFORMATION FOR SEQ ID NO:11:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 19 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
GTT	TCC CTC TTC TTG CTG T	1:
(2)	INFORMATION FOR SEQ ID NO 12:	
/	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	•
	(ii) MOLECULE TYPE: DNA	
1	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
TTT	TCT TTT GTC TTT GGG TAT	21
(2)	INFORMATION FOR SEQ ID NO:13:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA	

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCA ACT TAC AAG GCC TTT CTG

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 23 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single

Printed from Mimosa

	-								- 31	-						- (1)		
١	\																	
			(1	) TC	POLC	GY:	line	ear										
		(ii)	MOI	ECUI	E TY	PE:	DNA											
	,	(xi)	SEC	QUENC	E DE	ESCRI	PTIC	on: s	EQ I	D NO	:14:							
	CAT	CGT	TTC	CAT	GGC	TGC	TAG	GC									23	
	(2)	INFO	RMAI	TON	FOR	SEQ	ID N	10:15	5:									
		(i)	(À (E (C	LE 3) TY 3) SI	NGTH PE: RANE	IARAC I: 19 nucl EDNE GY:	bas eic SS:	e pa ació sino	irs 1									
		(ii)	MOL	ECUL	E TY	PE:	DNA											
		(xi)	SEQ	UENC	E DE	SCRI	PTIC	N: S	SEQ I	D NC	: 15:							
	GTT	TCC (	CTC	TTC	TTG	STG	T										19	
	(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	10 : 1,6	5:									
		(i)	(A (E (C	) LE 3) TY 3) ST	NGTH PE: RAND	IARAC I: 21 nucl EDNE OGY:	bas eid SS:	e pa acid sing	irs I									
	,	(ii)	MOL	ECUL	E TY	PE:	DNA											
N		(xi)	SEÇ	UENC	E DE	SCRI	PTIC	on: S	EO I	D NO	:16:							
/ 'I	ATA	ccc .	AAA	GAC	AAA	AGA	AAA									21		
	(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	JO:17	7:									
		(i)	(E (C	A) LE B) TY C) SI	ENGTH (PE : TRANI	ARAC i: 55 nucl DEDNE DGY:	0 ba .eic ESS:	ase p acio sino	pairs 1	, \	\					-		
		(ii)	MOI	ECUI	LE TY	PE:	DNA				\							
		(ix)	( P		ME/F	KEY:		549										
		(xi)	SEC	QUENC	CE DI	ESCRI	[PTIC	ON: S	SEQ I	D N	0:17	:	/	\				
	TCT Ser 1	TCC Ser	AAT Asn	TTG Leu	TCC Ser	TGG Trp	TTA Leu	TCG Ser	CTG Leu	GAT Asp 10	GTG Val	TCT Ser	GCG Ala	GCG Ala	TTT Phe 15	TAT Tyr		48
	CAT	ATT Ile	CCT Pro	CTT Leu 20	CAT	CCT Pro	GCT Ala	GCT Ala	ATG Met 25	CCT	CAT His	CTT Leu	CTT Leu	ATT Ile 30	ĢGT	TCT Ser		96
	TCT Ser	GGA Gly	TTA Leu	TCA Ser	AGG Arg	TAT Tyr	GTT Val	GCC Ala	CGT Arg	TTG Leu	TCC Ser	TCT Ser	AAT Asn	TCC Ser	AGG Arg	\ATC   le		144

- 32 -

			35					40					45				
	AAA Asn	AAC Asn 50	AAC Asn	ATG Met	CAA Gln	AAC <b>As</b> n	CTG Leu 55	CAC His	GAC Asp	TCC Ser	TGC Cys	TCA Ser 60	AGG Arg	CAA Gln	CTC Leu	TAC Tyr	192
	GTT Val 65	TCC Ser	CTC Leu	ATG Met	TTG Leu	CTG Leu 70	TAC Tyr	AAA Lys	ACC Thr	TAC Tyr	GGA Gly 75	GAG Glu	AAA Lys	TTG Leu	CAC His	CTG Leu 80	240
	ТАТ Туг	TCC Ser	CAT His	CCC Pro	ATC Ile 85	GTC Val	CTG Leu	GGC Gly	TTT Phe	CGC Arg 90	AAA Lys	ATA Ile	CCT Pro	ATG Met	GGA Gly 95	GTG Val	288
	GGC Gly	CTC Leu	AGT Ser	CCG Pro 100	TTT Phe	CTC Leu	TTG Leu	GCT Ala	CAG Gln 105	TTT Phe	ACT Thr	AGT Ser	GCC Ala	ATT Ile 110	TGT Cys	TCA Ser	336
	GTG Val	GTT Val	CGT Arg 115	AGG Arg	GCT Ala	TTC Phe	CCC Pro	CAC His 120	TGT Cys	TTG Leu	GCT Ala	TTC Phe	AGC Ser 125	TAT Tyr	ATG Met	GAT Asp	384
	GAT Asp	GTG Val 130	GTA Val	TTG Leu	GGG Gly	GCC Ala	AAG Lys 135	TCT Ser	GTA Val	CAG Gln	CAT His	CGT Arg 140	GAG Glu	GCC Ala	CTT Leu	TAT Tÿr	432
	ACC Thr 145	GCT Ala	GTT Val	ACC Thr	AAT Asn	TTT Phe 150	CTT	TTG Leu	TCT Ser	CTG Leu	GGT Gly 155	ATA Ile	CAT	TTA Leu	AAC Asn	CCT Pro 160	480
	AAC Asn	AAA Lys	ACA Thr	AAA Lys	AGA Arg 165	TGG Trp	GGT Gly	TAT Tyr	TCC Ser	CTA Leu 170	Asn	TTC Phe	ATG Met	GGT Gly	TAC Tyr 175	ATA Ile	528
)			AGT Ser														550
1	(2)	INF	ORMA	TION	FOR	SEO	ID	NO:1	8:								

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 183 amino acids

    - (B) TYPE: amino acid (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr
1 5 10 15

His Ile Pro Leu His Pro Ala Ala Met Pro His Leu Leu Ile Gly Ser 20 25 30

Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile 35

Asn Asn Asn Met Gln Asn Leu His Asp Ser Cys Ser Arg Gln Leu Tyr 50 60

Val Ser Leu Met Leu Leu Tyr Lys Thr Tyr Gly Glu Lys Leu His Leu 65 70 75 80

Tyr Ser His Pro Ile Val Leu Gly Phe Arg Lys Ile Pro Met Gly Val

- 33 -

gd A	Leu	Ser	Pro 100	Phe	Leu	Leu	Ala	Gln 105	Phe-	Thr	Ser	Ala	Ile 110	Cys	Ser
Val	Val	Arg 115	Arg	Ala	Phe	Pro	His 120	Cys	Leu	Ala	Phe	Ser 125	Tyr	Met	Asp
Asp	Va. 130	Val	Leu	Gly	Ala	Lys 135	Ser	Val	Gln	His	Arg 140	Glu	Ala	Leu	Tyr
Thr 145	Ala	Val	Thr	Asn	Phe 150	Leu	Leu	Ser	Leu	Gly 155	Ile	His	Leu	Asn	Pro 160
Asn	Lys	Thr	Lγs	Arg 165	Trp	Gly	Туr	Ser	Leu 170	Asn	Phe	Met	Gly	Tyr 175	Ile
Ile	Gly	Ser	Trp	Gly \	Thr	Leu									
(2)	INF	ORMA	rion	FOR	SEQ	ID 1	NO:1	9:							
	(2) INFORMATION FOR SEQ ID NO:19:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 550 base pairs  (B) TYPE: hucleic acid														***

(C) STRANDEDNESS: single (D) TOPOLOGY linear

(ii) MOLECULE TYPE:

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

T CT Le	T CC u Pr 1	A AT	T TG	T CC	T GG o Gl 5	т та у ту	T CG	G TG g Tr	G AT p Me 1	rG TG et Cy .0	T CT	G CG u Ar	G CG	y Fr	т .е .5	46
ATC Ile	ATA Ile	TTC Phe	CTC Leu	TTC Phe 20	ATC Ile	CTG Leu	CTG Leu	CTA Leu	TGC Cys 25	CTC Leu	ATC Ile	TTC Phe	TTA Leu	TTG Leu 30	GTT Val	94
CTT Leu	CTG Leu	GAT Asp	TAT Tyr 35	CAA Gln	GGT Gly	ATG Met	TTG Leu	CCC Pro 40	GTT Val	TGT Cys	CCT Pro	CTA Leu	ATT Ile 45	CCA Pro	GGA Gly	142
TCA Ser	ACA Thr	ACA Thr 50	ACA Thr	TGC Cys	AAA Lys	ACC Thr	TGC Cys 55	ACG Thr	ACT Thr	CCT Pro	GCT Ala	CAA Gln 60	GGC Gly	AAC Asn	TCT Ser	190
ACG Thr	TTT Phe 65	CCC Pro	TCA Ser	TGT Cys	TGC Cys	TGT Cys 70	ACA Thr	AAA Lys	CCT Pro	ACG Thr	GAG Glu 75	Arg	AAT Asn	TGC Cys	ACC Thr	238
TGT Cys 80	ATT Ile	CCC Pro	ATC Ile	CCA Pro	TCG Ser 85	TCC Ser	TGG Trp	GCT Ala	TTC Phe	GCA Ala 90	AAA Lys	TAC Tyr	CTA Leu	TGG Trp \	GAG Glu 95	2,86
TGG Trp	GCC Ala	TCA Ser	GTC Val	CGT Arg 100	Phe	TCT Ser	TGG Trp	CTC Leu	AGT Ser 105	Leu	CTA Leu	GTG Val	CCA Pro	TTT Phe 110	GTT Val	334
CAG Gln	TGG Trp	TTC Phe	GTA Val 115	Gly	CTT Leu	TCC Ser	CCC Pro	ACT Thr 120	Val	TGG Trp	CTT Leu	TCA Ser	GCT Ala 125	TIE	TEG	382

Printed from Mimosa

- 34 -

ATG Met	ATG Met	TGG Trp 130	TAT Tyr	TGG Trp	GGG Gly	CCA Pro	AGT Ser 135	CTG Leu	TAC Tyr	AGC Ser	ATC Ile	GTG Val 140	AGG Arg	CCC Pro	TTT Phe	430
ATA Ile	CCG Pro	CTG Leu	TTA Leu	CCA Pro	ATT Ile	TTC Phe 150	TTT Phe	TGT Cys	CTC Leu	TGG Trp	GTA Val 155	TAC Tyr	ATT Ile	TAA *	ACC Thr	478
CTA Leu 160	ACA Thr	AAA Lys	CAA Gln	AAA Lys	GAT Asp 165	GGG Gly	GTT Val	ATT Ile	CCC Pro	TAA * 170	ACT Thr	TCA Ser	TGG Trp	GTT Val	ACA Thr 175	526
TAN *	TTG Leu				GAA Glu											550

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 183 amino acids
  - (B) TYPE: amino acid (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile 10 Leu Pro Ile Cys Pro Gly

Ile Phe Leu Phe Ile Leu Leu Cys Leu Ile Phe Leu Leu Val Leu 25 30

Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly Ser

Thr Thr Thr Cys Lys Thr Cys Thr Thr Pro Ala Gln Gly Asn Ser Thr 50 60

Phe Pro Ser Cys Cys Cys Thr Lys Pro Thr Glu Arg Asn Cys Thr Cys 65 70 75 80

Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Lys Tyr Leu Trp Glu Trp 85 90 95

Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln
100 105 110

Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Ala Ile Trp Met

Met Trp Tyr Trp Gly Pro Ser Leu Tyr Ser Ile Val Arg Pro Phe Ile 130

Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile

Thr Lys Gln Lys Asp Gly Val Ile Pro 165 Thr Ser Trp Val Thr

Leu Glu Val Gly Glu His Cys 180